

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/300,494

CRF Processing Date: 3/30/95 #
Edited by: AM
Verified by: STIC (STIC staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
Seq. 8 had a "10" in the SEQ ID NO field

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other:

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

Andrew C. Hiatt, Floyd Rose

(ii) TITLE OF INVENTION: ENZYME CATALYZED TEMPLATE-INDEPENDENT CREATION OF PHOSPHODIESTER BONDS USING PROTECTED NUCLEOTIDES

12 (iii) NUMBER OF SEQUENCES: 8

3

(iv) CORRESPONDENCE ADDRESS:

Lyon & Lyon
633 West Fifth Street
Suite 4700
Los Angeles
California
U.S.A.
90071

(v) COMPUTER READABLE FORM:

3.5" Diskette, 1.44 Mb
storage
IBM Compatible
IBM P.C. DOS 5.0
Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/300,484
(B) FILING DATE: September 1, 1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below: none

(viii) ATTORNEY/AGENT INFORMATION:

Guise, Jeffrey W.

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/300,484

DATE: 03/30/95
TIME: 21:01:23

INPUT SET: S3019.raw

17 (B) REGISTRATION NUMBER: 1511234/613
18 (C) REFERENCE/DOCKET NUMBER: 1207/145

19
20 (ix) TELECOMMUNICATION INFORMATION:

21 (A) TELEPHONE: (619) 552-8400
22 (B) TELEFAX: (619) 552-0159
23 (C) TELEX: 67-3510

24
25 (2) INFORMATION FOR SEQ ID NO: 1:

26 (i) SEQUENCE CHARACTERISTICS:

27 (A) LENGTH: 12
28 (B) TYPE: nucleic acid
29 (C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

31 (ix) FEATURE:

32 (D) OTHER INFORMATION: base number 12 is m7g

33 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

34 CCCCCCCCCC CG

12

35 (2) INFORMATION FOR SEQ ID NO: 2:

36 (i) SEQUENCE CHARACTERISTICS:

37 (A) LENGTH: 19
38 (B) TYPE: nucleic acid
39 (C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

41 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

42 CCCCCCCCCC CCCCCTGCCA

19

43 (2) INFORMATION FOR SEQ ID NO: 3:

44 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 20
46 (B) TYPE: nucleic acid
47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear

49

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/300,484DATE: 03/30/95
TIME: 21:01:28

INPUT SET: S3019.raw

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182

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTGCATGCA

9

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTGCATGCAG

10

*****PREVIOUSLY ERRORED SEQUENCES- EDITED*****

166 (2) INFORMATION FOR SEQ ID NO: 8:

167

168 (i) SEQUENCE CHARACTERISTICS:

169

170 (A) LENGTH: 10

171 (B) TYPE: nucleic acid

172 (C) STRANDEDNESS: single

173 (D) TOPOLOGY: linear

174

175 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

176

177 CTGCATGCAG

10

178

179

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181

182

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/300,484

DATE: 03/30/95
TIME: 21:01:31

INPUT SET: S3019.raw

Line

Error

Original Text

INPUT SET: S3019.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Andrew C. Hiatt, Floyd Rose

(ii) TITLE OF INVENTION: ENZYME CATALYZED TEMPLATE-INDEPENDENT CREATION OF PHOSPHODIESTER BONDS USING PROTECTED NUCLEOTIDES

(iii) NUMBER OF SEQUENCES:

8

(iv) CORRESPONDENCE ADDRESS:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/300,484
(B) FILING DATE: September 1, 1994
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

Prior applications total,
including application
described below:

(viii) ATTORNEY/AGENT INFORMATION:

INPUT SET: S3019.raw

46 (A) NAME: Guise, Jeffrey, W.
47 (B) REGISTRATION NUMBER: 34,613
48 (C) REFERENCE/DOCKET NUMBER: 207/145

49
50 (ix) TELECOMMUNICATION INFORMATION:

51
52 (A) TELEPHONE: (619) 552-8400
53 (B) TELEFAX: (619) 552-0159
54 (C) TELEX: 67-3510 (2) INFORMATION FOR SEQ ID NO:
55

--> 56 (i) SEQUENCE CHARACTERISTICS:

57
--> 58 (A) LENGTH: 12
--> 59 (B) TYPE: nucleic acid
--> 60 (C) STRANDEDNESS: single
--> 61 (D) TOPOLOGY: linear

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--> 63 (ix) Features:

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--> 65 (D) Other Information: base number 12 is m7g
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67

--> 68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69
70 CCCCCCCCCC CG
71
72
73

12

remove
hard
page
break
code

ERRORED SEQUENCES FOLLOW:

164 (2) INFORMATION FOR SEQ ID NO: 8:

165
166 (i) SEQUENCE CHARACTERISTICS:

167
168 (A) LENGTH: 10
169 (B) TYPE: nucleic acid
170 (C) STRANDEDNESS: single
171 (D) TOPOLOGY: linear

172
--> 173 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 10

174
175 CTGCATGCAG
176
177
178
179

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/300,484DATE: 03/30/95
TIME: 15:57:29

INPUT SET: S3019.raw

Line	Error	Original Text
12	Number of Sequences (8) Doesn't Equal Actual Count (7)	(iii) NUMBER OF SEQUENCES: 8
56	Unknown or Misplaced Identifier	(i) SEQUENCE CHARACTERISTICS:
58	Unknown or Misplaced Identifier	(A) LENGTH: 12
59	Unknown or Misplaced Identifier	(B) TYPE: nucleic acid
60	Unknown or Misplaced Identifier	(C) STRANDEDNESS: single
61	Unknown or Misplaced Identifier	(D) TOPOLOGY: linear
63	Unknown or Misplaced Identifier	(ix) Features:
65	Unknown or Misplaced Identifier	(D) Other Information: base number 12 is m7g
68	Unknown or Misplaced Identifier	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
173	Wrong Sequence Number	(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 10: